



PCT10

## RAW SEQUENCE LISTING

DATE: 11/18/2002

PATENT APPLICATION: US/10/030,194

TIME: 15:02:28

Input Set : A:\EP.txt

Output Set: N:\CRF4\11182002\J030194.raw

7 <110> APPLICANT: RENARD, MICHEL  
 10 DELOURME, REGINE  
 13 BARRET, PIERRE  
 16 BRUNEL, DOMINIQUE  
 19 FROGER, NICOLE  
 22 TANGUY, XAVIER  
 28 <120> TITLE OF INVENTION: MUTANT GENE OF THE GRAS FAMILY AND PLANTS WITH REDUCED  
 29 DEVELOPMENT CONTAINING SAID MUTANT GENE  
 35 <130> FILE REFERENCE: 218874US0PCT  
 41 <140> CURRENT APPLICATION NUMBER: 10/030,194  
 44 <141> CURRENT FILING DATE: 2002-02-04  
 50 <150> PRIOR APPLICATION NUMBER: PCT/FR00/02216  
 53 <151> PRIOR FILING DATE: 2000-08-02  
 59 <150> PRIOR APPLICATION NUMBER: FR 9910023  
 62 <151> PRIOR FILING DATE: 1999-08-02  
 E--> 68 <160> NUMBER OF SEQ ID NOS: 63 *see below*  
 74 <170> SOFTWARE: PatentIn version 3.1

## ERRORED SEQUENCES

Does Not Comply  
Corrected Diskette Needed

714 <210> SEQ ID NO: 3  
 717 <211> LENGTH: 1779 *last sequence in submitted file*  
 720 <212> TYPE: DNA  
 723 <213> ORGANISM: Brassica napus  
 729 <220> FEATURE:  
 732 <221> NAME/KEY: CDS  
 735 <222> LOCATION: (60)..(1778) *589 (see p.2)*  
 738 <223> OTHER INFORMATION:  
 W- 745 <400> 3  
 747 caaccagaa caaaaccaga ccgatctgag agattaacta tatcttaacc agatcagaa 59  
 751 atg aag agg gat ctt cat cag ttc caa ggt ccc aac cac ggg aca tca 107  
 753 Met Lys Arg Asp Leu His Gln Phe Gln Gly Pro Asn His Gly Thr Ser  
 755 1 5 10 15  
 759 atc gcc ggt tct tcc act tct tcc cct gcg gtg ttt ggt aaa gac aag 155  
 761 Ile Ala Gly Ser Ser Thr Ser Ser Pro Ala Val Phe Gly Lys Asp Lys  
 763 20 25 30  
 767 atg atg atg gtc aaa gaa gaa gaa gac gac gag ctt cta gga gtc ttg 203  
 769 Met Met Met Val Lys Glu Glu Glu Asp Asp Glu Leu Leu Gly Val Leu  
 771 35 40 45  
 775 ggt tac aag gtt agg tct tct gag atg gct gag gtt gcg ttg aaa ctc 251  
 777 Gly Tyr Lys Val Arg Ser Ser Glu Met Ala Glu Val Ala Leu Lys Leu  
 779 50 55 60

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783 gag cag ctt gag acg atg atg ggt aac gct caa gaa gac ggt tta gct      299
785 Glu Gln Leu Glu Thr Met Met Gly Asn Ala Gln Glu Asp Gly Leu Ala
787 65                      70                      75                      80
791 cac ctc gcg acg gat act gtt cat tac aac ccc gct gag ctt tac tcg      347
793 His Leu Ala Thr Asp Thr Val His Tyr Asn Pro Ala Glu Leu Tyr Ser
795                      85                      90                      95
799 tgg ctt gat aac atg ctc acg gag ctt aac cca ccc gct gca acg acc      395
801 Trp Leu Asp Asn Met Leu Thr Glu Leu Asn Pro Pro Ala Ala Thr Thr
803                      100                      105                      110
807 gga tct aac gct ttg aac ccg gag att aat aat aat aat aat aac tcg      443
809 Gly Ser Asn Ala Leu Asn Pro Glu Ile Asn Asn Asn Asn Asn Asn Ser
811                      115                      120                      125
815 ttt ttc acc gga ggc gac ctc aaa gcg att cct gga aac gcg gtt tgt      491
817 Phe Phe Thr Gly Gly Asp Leu Lys Ala Ile Pro Gly Asn Ala Val Cys
819                      130                      135                      140
823 cgc aga tct aat cag ttc gcg ttt gcg gtt gat tcg tcg agt aat aag      539
825 Arg Arg Ser Asn Gln Phe Ala Phe Ala Val Asp Ser Ser Ser Asn Lys
827 145                      150                      155                      160
831 cgt ttg aaa ccg tcc tcg agc cct gat tcg atg gtt aca tct cca tca      587
833 Arg Leu Lys Pro Ser Ser Ser Pro Asp Ser Met Val Thr Ser Pro Ser
E--> 835                      165                      170

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the  
correct  
nucleotide  
total  
195 ← insert

**VERIFICATION SUMMARY**

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Input Set : A:\EP.txt

Output Set: N:\CRF4\11182002\J030194.raw

L:111 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:104  
L:745 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:738  
L:835 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:835 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1779 Found:587 SEQ:3  
L:68 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (6) Counted (3)